IN THE UNITED STATES RECEIVING OFFICE (RO/US)

BOX PCT

In re International Patent Application of

DUKE UNIVERSITY ET AL

Agent's File Ref: 1579-379

International Application No: PCT/US99/17678

International Filing Date: 05 August 1999

For: URATE OXIDASE

19 November 1999

United States Receiving Office Honorable Commissioner of Patents and Trademarks Washington, D.C. 20231

Response to Correct Defects in International Application

Dear Sirs,

Attached is a printed sequence listing for this application and a copy of the computer readable form on a 3.5" disk in the attached envelope.

In accordance with 37 CFR 1.821-1.825, I hereby state that the content of the paper and computer-readable copies of the sequence listing submitted in accordance with 37 CFR 1.821(c) and (e), respectively, are the same. I hereby state that the submission, filed in accordance with 37 CFR 1.821(g), does not introduce new matter.

Respectfully submitted,

NIXON & VANDERHYE P.C.

8th Floor 1100 North Glebe Road Arlington, Virginia 22201-4714

SEQUENCE LISTING

<110> HERSHFIELD, MICHAEL S. KELLY, SUSAN J.							
<120> URATE OXIDASE							
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<140> PCT/US99/17678 <141> 1999-08-05							
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cag Gln 145	r TTG	agg Arg	aat Asn	gga Gly	cct Pro 150	Pro	gtc Val	att	cat	tct Ser 155	Gly	ato Ile	aaa Lys	gac Asp	cta Leu 160	480
aaa Lys	gtc Val	ttg Leu	aaa Lys	aca Thr 165	Thr	cag Gln	tct Ser	ggc	ttt Phe 170	Glu	gga Gly	ttc Phe	atc Ile	aag Lys 175	gac Asp	528
cag Gln	ttc Phe	acc Thr	acc Thr 180	Leu	cct Pro	gag Glu	gtg Val	aag Lys 185	gac Asp	cgg Arg	tgc Cys	ttt Phe	gcc Ala 190	acc Thr	caa Gln	576
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gcc Ala	acc Thr 210	tgg Trp	gac Asp	act Thr	gtt Val	agg Arg 215	agc Ser	att Ile	gtc Val	ctg Leu	cag Gln 220	aaa Lys	ttt Phe	gct Ala	Gly ggg	672
ccc Pro 225	tat Tyr	gac Asp	aaa Lys	ggc Gly	gag Glu 230	tac Tyr	tca Ser	ccc Pro	tct Ser	gtg Val 235	cag Gln	aag Lys	acc Thr	ctc Leu	tat Tyr 240	720
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gaa Glu	atc Ile	agc Ser	ctg Leu 260	cca Pro	aac Asn	att Ile	cac His	tac Tyr 265	ttc Phe	aat Asn	ata Ile	gac Asp	atg Met 270	tcc Ser	aaa Lys	816
atg Met	ggt Gly	ctg Leu 275	atc Ile	aac Asn	aag Lys	gaa Glu	gag Glu 280	gtc Val	ttg Leu	ctg Leu	cca Pro	tta Leu 285	gac Asp	aat Asn	cca Pro	864
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305																
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Arg	Asp	Gly 35	Lys	Tyr	His	Ser	Ile 40	Lys	Glu	Val	Ala	Thr 45		Val	Gln	
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- 31

Phe Lys Gly Ile Lys Ser Ile Glu Thr Phe Ala Val Thr Ile Cys Glu

His Phe Leu Ser Ser Phe Lys His Val Ile Arg Ala Gln Val Tyr Val 105 Glu Glu Val Pro Trp Lys Arg Phe Glu Lys Asn Gly Val Lys His Val His Ala Phe Ile Tyr Thr Pro Thr Gly Thr His Phe Cys Glu Val Glu 130 Gln Ile Arg Asn Gly Pro Pro Val Ile His Ser Gly Ile Lys Asp Leu Lys Val Leu Lys Thr Thr Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp 170 Gln Phe Thr Thr Leu Pro Glu Val Lys Asp Arg Cys Phe Ala Thr Gln Val Tyr Cys Lys Trp Arg Tyr His Gln Gly Arg Asp Val Asp Phe Glu Ala Thr Trp Asp Thr Val Arg Ser Ile Val Leu Gln Lys Phe Ala Gly 215 Pro Tyr Asp Lys Gly Glu Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr 235 Asp Ile Gln Val Leu Ser Leu Ser Arg Val Pro Glu Ile Glu Asp Met 245 Glu Ile Ser Leu Pro Asn Ile His Tyr Phe Asn Ile Asp Met Ser Lys 265 Met Gly Leu Ile Asn Lys Glu Glu Val Leu Leu Pro Leu Asp Asn Pro 285 Tyr Gly Lys Ile Thr Gly Thr Val Lys Arg Lys Leu Ser Ser Arg Leu 295 <210> 3 <211> 915 <212> DNA <213> Artificial Sequence <220> <221> CDS <222> (1)..(915) <223> Description of Artificial Sequence:pks chimera <400> 3 atg gct cat tac cgt aat gac tac aaa aag aat gat gag gta gag ttt 48 Met Ala His Tyr Arg Asn Asp Tyr Lys Lys Asn Asp Glu Val Glu Phe 15 gtc cga act ggc tat ggg aag gat atg ata aaa gtt ctc cat att cag Val Arg Thr Gly Tyr Gly Lys Asp Met Ile Lys Val Leu His Ile Gln

1.6

cga Arg	a gat g Asp	gga Gly 35	Y Lys	a tat	cac r His	ago Sei	att Ile 40	: Lys	gaq Glu	g gtg ı Val	g gca L Ala	act Thr 45	Ser	gtg Val	caa Gln	144
cto Lev	g act 1 Thr 50	Let	g ago 1 Ser	tco Ser	c aaa C Lys	a aaa 5 Lys 55	Asp	tac Tyr	cto Lev	g cat 1 His	gga Gly 60	Asp	aat Asn	tca Ser	gat Asp	192
gto Val 65	. TIE	e cct	aca Thr	gac Asp	acc Thr 70	Ile	aag Lys	aac Asn	aca Thr	gtt Val 75	Asn	gto Val	ctg Leu	gcg Ala	aag Lys 80	240
ttc Phe	aaa Lys	ggc Gly	ato Ile	aaa Lys 85	Ser	ata Ile	gaa Glu	act Thr	ttt Phe 90	: Ala	gtg Val	act Thr	atc Ile	tgt Cys 95	gag Glu	288
cat His	ttc Phe	ctt Leu	tct Ser 100	Ser	ttc Phe	aag Lys	cat His	gtc Val 105	atc Ile	aga Arg	gct Ala	caa Gln	gtc Val 110	tat Tyr	gtg Val	336
gaa Glu	gaa Glu	gtt Val 115	cct Pro	tgg Trp	aag Lys	cgt Arg	ttt Phe 120	gaa Glu	aag Lys	aat Asn	gga Gly	gtt Val 125	aag Lys	cat His	gtc Val	384
cat His	gca Ala 130	Pne	att Ile	tat Tyr	act Thr	cct Pro 135	act Thr	gga Gly	acg Thr	cac His	ttc Phe 140	tgt Cys	gag Glu	gtt Val	gaa Glu	432
cag Gln 145	ata Ile	agg Arg	aat Asn	gga Gly	cct Pro 150	cca Pro	gtc Val	att Ile	cat His	tct Ser 155	gga Gly	atc Ile	aaa Lys	gac Asp	cta Leu 160	480
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cag Gln	ttc Phe	acc Thr	acc Thr 180	ctc Leu	cct Pro	gag Glu	gtg Val	aag Lys 185	gac Asp	cgg Arg	tgc Cys	ttt Phe	gcc Ala 190	acc Thr	caa Gln	576
gtg Val	tac Tyr	tgc Cys 195	aaa Lys	tgg Trp	cgc Arg	tac Tyr	cac His 200	cag Gln	ggc Gly	aga Arg	gat Asp	gtg Val 205	gac Asp	ttt Phe	gag Glu	624
gcc Ala	acc Thr 210	tgg Trp	gac Asp	act Thr	gtt Val	agg Arg 215	agc Ser	att Ile	gtc Val	ctg Leu	cag Gln 220	aaa Lys	ttt Phe	gct Ala	Gly ggg	672
CCC Pro 225	tat Tyr	gac Asp	aaa Lys	ggc Gly	gag Glu 230	tac Tyr	tcg Ser	ccc Pro	tct Ser	gtc Val 235	cag Gln	aag Lys	aca Thr	ctc Leu	tat Tyr 240	720
gac Asp	atc Ile	cag Gln	gtg Val	ctc Leu 245	acc Thr	ctg Leu	ggc Gly	Gln	gtt Val 250	cct Pro	gag Glu	ata Ile	gaa Glu	gat Asp 255	atg Met	768
GIU	TIE	ser	ctg Leu 260	Pro	Asn	ile	His	Tyr 265	Leu	Asn	Ile	Asp	Met 270	Ser	Lys	816
atg Met	GTA	ctg Leu 275	atc Ile	aac Asn	aag Lys	gaa Glu	gag Glu 280	gtc Val	ttg Leu	cta Leu	Pro	tta Leu 285	gac Asp	aat Asn	cca Pro	864

912

915

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Met Gly Leu Ile Asn Lys Glu Glu Val Leu Leu Pro Leu Asp Asn Pro 275 280 285

Tyr Gly Lys Ile Thr Gly Thr Val Lys Arg Lys Leu Ser Ser Arg Leu 290 295 300

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<211> 304

<212> PRT

<213> Artificial Sequence

<220>

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Val Arg Thr Gly Tyr Gly Lys Asp Met Val Lys Val Leu His Ile Gln 20 25 30

Arg Asp Gly Lys Tyr His Ser Ile Lys Glu Val Ala Thr Ser Val Gln
35 40 45

Leu Thr Leu Ser Ser Lys Lys Asp Tyr Leu His Gly Asp Asn Ser Asp 50 55 60

Ile Ile Pro Thr Asp Thr Ile Lys Asn Thr Val His Val Leu Ala Lys 65 70 75 80

Phe Lys Gly Ile Lys Ser Ile Glu Ala Phe Gly Val Asn Ile Cys Glu 85 90 95

Tyr Phe Leu Ser Ser Phe Asn His Val Ile Arg Ala Gln Val Tyr Val
100 105 110

Glu Glu Ile Pro Trp Lys Arg Leu Glu Lys Asn Gly Val Lys His Val 115 120 125

His Ala Phe Ile His Thr Pro Thr Gly Thr His Phe Cys Glu Val Glu 130 135 140

Gln Leu Arg Ser Gly Pro Pro Val Ile His Ser Gly Ile Lys Asp Leu 145 150 155 160

Lys Val Leu Lys Thr Thr Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp 165 170 175

Gln Phe Thr Thr Leu Pro Glu Val Lys Asp Arg Cys Phe Ala Thr Gln 180 185 190

Val Tyr Cys Lys Trp Arg Tyr His Gln Cys Arg Asp Val Asp Phe Glu 195 200 205

Ala Thr Trp Gly Thr Ile Arg Asp Leu Val $^{\circ}$ Leu Glu Lys Phe Ala Gly 210 215 220

Pro Tyr Asp Lys Gly Glu Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr 225 230 235 240

Asp Ile Gln Val Leu Ser Leu Ser Arg Val Pro Glu Ile Glu Asp Met 245 250 255

Glu Ile Ser Leu Pro Asn Ile His Tyr Phe Asn Ile Asp Met Ser Lys 260 265 270 Met Gly Leu Ile Asn Lys Glu Glu Val Leu Leu Pro Leu Asp Asn Pro 275 280 285

Tyr Gly Lys Ile Thr Gly Thr Val Lys Arg Lys Leu Ser Ser Arg Leu 290 295 300

<210> 6 <211> 304

<212> PRT

<213> baboon

<400> 6
Met Ala Asp Tyr His Asn Asn Tyr Lys Lys Asn Asp Glu Leu Glu Phe
1 5 10 15

Val Arg Thr Gly Tyr Gly Lys Asp Met Val Lys Val Leu His Ile Gln 20 25 30

Arg Asp Gly Lys Tyr His Ser Ile Lys Glu Val Ala Thr Ser Val Gln 35 40 45

Leu Thr Leu Ser Ser Lys Lys Asp Tyr Leu His Gly Asp Asn Ser Asp 50 60

Ile Ile Pro Thr Asp Thr Ile Lys Asn Thr Val His Val Leu Ala Lys 65 70 75 80

Phe Lys Gly Ile Lys Ser Ile Glu Ala Phe Gly Val Asn Ile Cys Glu 85 90 95

Tyr Phe Leu Ser Ser Phe Asn His Val Ile Arg Ala Gln Val Tyr Val 100 105 110

Glu Glu Ile Pro Trp Lys Arg Leu Glu Lys Asn Gly Val Lys His Val 115 120 125

His Ala Phe Ile His Thr Pro Thr Gly Thr His Phe Cys Glu Val Glu 130 135 140

Gln Leu Arg Ser Gly Pro Pro Val Ile His Ser Gly Ile Lys Asp Leu 145 150 155 160

Lys Val Leu Lys Thr Thr Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp 165 170 175

Gln Phe Thr Thr Leu Pro Glu Val Lys Asp Arg Cys Phe Ala Thr Gln 180 185 190

Val Tyr Cys Lys Trp Arg Tyr His Gln Cys Arg Asp Val Asp Phe Glu 195 200 205

Ala Thr Trp Gly Thr Ile Arg Asp Leu Val Leu Glu Lys Phe Ala Gly
210 215 220

Pro Tyr Asp Lys Gly Glu Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr 225 230 235 240

Asp Ile Gln Val Leu Ser Leu Ser Arg Val Pro Glu Ile Glu Asp Met 245 250 255

Glu Ile Ser Leu Pro Asn Ile His Tyr Phe Asn Ile Asp Met Ser Lys
260 265 270

Met Gly Leu Ile Asn Lys Glu Glu Val Leu Leu Pro Leu Asp Asn Pro 275 280 285

Tyr Gly Lys Ile Thr Gly Thr Val Lys Arg Lys Leu Ser Ser Arg Leu 290 295 300

<210> 7

<211> 304

<212> PRT

<213> pig

<400> 7

Met Ala His Tyr Arg Asn Asp Tyr Lys Lys Asn Asp Glu Val Glu Phe 1 5 10 15

Val Arg Thr Gly Tyr Gly Lys Asp Met Ile Lys Val Leu His Ile Gln 20 25 30

Arg Asp Gly Lys Tyr His Ser Ile Lys Glu Val Ala Thr Ser Val Glu 35 40 45

Leu Thr Leu Ser Ser Lys Lys Asp Tyr Leu His Gly Asp Asn Ser Asp 50 55 60

Val Ile Pro Thr Asp Thr Ile Lys Asn Thr Val Asn Val Leu Ala Lys 65 70 75 80

Phe Lys Gly Ile Lys Ser Ile Glu Thr Phe Ala Val Thr Ile Cys Glu 85 90 95

His Phe Leu Ser Ser Phe Lys His Val Ile Arg Ala Gln Val Tyr Val

Glu Glu Val Pro Trp Lys Arg Phe Glu Lys Asn Gly Val Lys His Val 115 120 125

His Ala Phe Ile Tyr Thr Pro Thr Gly Thr His Phe Cys Glu Val Glu 130 135 140

Gln Ile Arg Asn Gly Pro Pro Val Ile His Ser Gly Ile Lys Asp Leu 145 150 155 160

Lys Val Leu Lys Thr Thr Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp 165 170 175

Gln Phe Thr Thr Leu Pro Glu Val Lys Asp Arg Cys Phe Ala Thr Gln 180 185 190

Val Tyr Cys Lys Trp Arg Tyr His Gln Gly Arg Asp Val Asp Phe Glu 195 200 205

Ala Thr Trp Asp Thr Val Arg Ser Ile Val Leu Gln Lys Phe Ala Gly 210 215 220

Pro Tyr Asp Lys Gly Glu Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr 225 230 235 240

Asp Ile Gln Val Leu Thr Leu Gly Gln Val Pro Glu Ile Glu Asp Met 245 250 255

Glu Ile Ser Leu Pro Asn Ile His Tyr Leu Asn Ile Asp Met Ser Lys 260 265 270

Met Gly Leu Ile Asn Lys Glu Glu Val Leu Leu Pro Leu Asp Asn Pro 275 280 285

Tyr Gly Arg Ile Thr Gly Thr Val Lys Arg Lys Leu Thr Ser Arg Leu 290 295 300

<210> 8

<211> 298

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PBC amino truncated

<400> 8

Asp Tyr Lys Lys Asn Asp Glu Val Glu Phe Val Arg Thr Gly Tyr Gly 1 5 10 15

Lys Asp Met Ile Lys Val Leu His Ile Gln Arg Asp Gly Lys Tyr His
20 25 30

Ser Ile Lys Glu Val Ala Thr Ser Val Gln Leu Thr Leu Ser Ser Lys 35 40 45

Lys Asp Tyr Leu His Gly Asp Asn Ser Asp Val Ile Pro Thr Asp Thr 50 55 60

Ile Lys Asn Thr Val Asn Val Leu Ala Lys Phe Lys Gly Ile Lys Ser 65 70 75 80

Ile Glu Thr Phe Ala Val Thr Ile Cys Glu His Phe Leu Ser Ser Phe 85 90 95

Lys His Val Ile Arg Ala Gln Val Tyr Val Glu Glu Val Pro Trp Lys
100 105 110

Arg Phe Glu Lys Asn Gly Val Lys His Val His Ala Phe Ile Tyr Thr 115 120 125

Pro Thr Gly Thr His Phe Cys Glu Val Glu Gln Ile Arg Asn Gly Pro 130 135 140

Pro Val Ile His Ser Gly Ile Lys Asp Leu Lys Val Leu Lys Thr Thr 145 150 155 160

Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp Gln Phe Thr Thr Leu Pro 165 170 175

Glu Val Lys Asp Arg Cys Phe Ala Thr Gln Val Tyr Cys Lys Trp Arg 180 185 190

Tyr His Gln Gly Arg Asp Val Asp Phe Glu Ala Thr Trp Asp Thr Val 195 200 205

Arg Ser Ile Val Leu Gln Lys Phe Ala Gly Pro Tyr Asp Lys Gly Glu 210 215 220 Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr Asp II'e Gln Val Leu Ser 225 235 240

Leu Ser Arg Val Pro Glu Ile Glu Asp Met Glu Ile Ser Leu Pro Asn 245 250 255

Ile His Tyr Phe Asn Ile Asp Met Ser Lys Met Gly Leu Ile Asn Lys 260 265 270

Glu Glu Val Leu Leu Pro Leu Asp Asn Pro Tyr Gly Lys Ile Thr Gly 275 280 285

Thr Val Lys Arg Lys Leu Ser Ser Arg Leu 290 295

<210> 9

<211> 301

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PBC carboxy truncated

<400> 9

Met Ala His Tyr Arg Asn Asp Tyr Lys Lys Asn Asp Glu Val Glu Phe
1 5 10 15

Val Arg Thr Gly Tyr Gly Lys Asp Met Ile Lys Val Leu His Ile Gln
20 25 30

Arg Asp Gly Lys Tyr His Ser Ile Lys Glu Val Ala Thr Ser Val Gln 35 40 45

Leu Thr Leu Ser Ser Lys Lys Asp Tyr Leu His Gly Asp Asn Ser Asp 50 55 60

Val Ile Pro Thr Asp Thr Ile Lys Asn Thr Val Asn Val Leu Ala Lys 65 70 75 80

Phe Lys Gly Ile Lys Ser Ile Glu Thr Phe Ala Val Thr Ile Cys Glu 85 90 95

His Phe Leu Ser Ser Phe Lys His Val Ile Arg Ala Gln Val Tyr Val 100 105 110

Glu Glu Val Pro Trp Lys Arg Phe Glu Lys Asn Gly Val Lys His Val 115 120 125

His Ala Phe Ile Tyr Thr Pro Thr Gly Thr His Phe Cys Glu Val Glu 130 135 140

Gln Ile Arg Asn Gly Pro Pro Val Ile His Ser Gly Ile Lys Asp Leu 145 150 155 160

Lys Val Leu Lys Thr Thr Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp 165 170 175

Gln Phe Thr Thr Leu Pro Glu Val Lys Asp Arg Cys Phe Ala Thr Gln 180 185 190

Val Tyr Cys Lys Trp Arg Tyr His Gln Gly Arg Asp Val Asp Phe Glu 195 200 205 Ala Thr Trp Asp Thr Val Arg Ser Ile Val Leu Gln Lys Phe Ala Gly 210 215 220

Pro Tyr Asp Lys Gly Glu Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr 225 230 235 240

Asp Ile Gln Val Leu Ser Leu Ser Arg Val Pro Glu Ile Glu Asp Met 245 250 255

Glu Ile Ser Leu Pro Asn Ile His Tyr Phe Asn Ile Asp Met Ser Lys 260 265 270

Met Gly Leu Ile Asn Lys Glu Glu Val Leu Leu Pro Leu Asp Asn Pro 275 280 285

Tyr Gly Lys Ile Thr Gly Thr Val Lys Arg Lys Leu Ser 290 295 300

<210> 10

<211> 298

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PKS carboxy truncated

<400> 10

Asp Tyr Lys Lys Asn Asp Glu Val Glu Phe Val Arg Thr Gly Tyr Gly 1 5 10 15

Lys Asp Met Ile Lys Val Leu His Ile Gln Arg Asp Gly Lys Tyr His
20 25 30

Ser Ile Lys Glu Val Ala Thr Ser Val Gln Leu Thr Leu Ser Ser Lys 35 40 45

Lys Asp Tyr Leu His Gly Asp Asn Ser Asp Val Ile Pro Thr Asp Thr 50 55 60

Ile Lys Asn Thr Val Asn Val Leu Ala Lys Phe Lys Gly Ile Lys Ser 65 70 75 80

Ile Glu Thr Phe Ala Val Thr Ile Cys Glu His Phe Leu Ser Ser Phe
85 90 95

Lys His Val Ile Arg Ala Gln Val Tyr Val Glu Glu Val Pro Trp Lys 100 105 110

Arg Phe Glu Lys Asn Gly Val Lys His Val His Ala Phe Ile Tyr Thr
115 120 125

Pro Thr Gly Thr His Phe Cys Glu Val Glu Gln Ile Arg Asn Gly Pro 130 135

Pro Val Ile His Ser Gly Ile Lys Asp Leu Lys Val Leu Lys Thr Thr 145 150 155 160

Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp Gln Phe Thr Thr Leu Pro 165 170 175

Glu Val Lys Asp Arg Cys Phe Ala Thr Gln Val Tyr Cys Lys Trp Arg 180 185 190 Tyr His Gln Gly Arg Asp Val Asp the Glu Ala Thr Trp Asp Thr Val

Arg Ser Ile Val Leu Gln Lys Phe Ala Gly Pro Tyr Asp Lys Gly Glu 210

Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr Asp Ile Gln Val Leu Thr 240 225

Leu Gly Gln Val Pro Glu Ile Glu Asp Met Glu Ile Ser Leu Pro Asn 255

Ile His Tyr Leu Asn Ile Asp Met Ser Lys Met Gly Leu Ile Asn Lys 270

Glu Glu Val Leu Leu Pro Leu Asp Asn Pro Tyr Gly Lys Ile Thr Gly 285

Thr Val Lys Arg Lys Leu Ser Ser Arg Leu 295

<210> 11

<211> 301

<213> Artificial Sequence

Description of Artificial Sequence:PKS carboxy truncated

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Arg Asp Gly Lys Tyr His Ser Ile Lys Glu Val Ala Thr Ser Val Gln 45

Leu Thr Leu Ser Ser Lys Lys Asp Tyr Leu His Gly Asp Asn Ser Asp 55

Val Ile Pro Thr Asp Thr Ile Lys Asn Thr Val Asn Val Leu Ala Lys 80 65

Phe Lys Gly Ile Lys Ser Ile Glu Thr Phe Ala Val Thr Ile Cys Glu 95

His Phe Leu Ser Ser Phe Lys His Val Ile Arg Ala Gln Val Tyr Val

Glu Glu Val Pro Trp Lys Arg Phe Glu Lys Asn Gly Val Lys His Val

His Ala Phe Ile Tyr Thr Pro Thr Gly Thr His Phe Cys Glu Val Glu

Gln Ile Arg Asn Gly Pro Pro Val Ile His Ser Gly Ile Lys Asp Leu 160

Lys Val Leu Lys Thr Thr Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp 175

Gln Phe Thr Thr Leu Pro Glu Val Lys Asp Arg Cys Phe Ala Thr Gln 180 185 190

Val Tyr Cys Lys Trp Arg Tyr His Gln Gly Arg Asp Val Asp Phe Glu 195 200 205

Ala Thr Trp Asp Thr Val Arg Ser Ile Val Leu Gln Lys Phe Ala Gly 210 215 220

Pro Tyr Asp Lys Gly Glu Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr 225 230 235 240

Asp Ile Gln Val Leu Thr Leu Gly Gln Val Pro Glu Ile Glu Asp Met 245 250 255

Glu Ile Ser Leu Pro Asn Ile His Tyr Leu Asn Ile Asp Met Ser Lys 260 265 270

Met Gly Leu Ile Asn Lys Glu Glu Val Leu Leu Pro Leu Asp Asn Pro 275 280 285

Tyr Gly Lys Ile Thr Gly Thr Val Lys Arg Lys Leu Ser 290 295 300

	Serial No.: PCT US99 1767 Atty: Applicant: Dake University Title: PCT 10399 17678 Amendment Pages Specification Claims Sheets Drawings: Formal Informal Declaration (Pages) Assignment Priority Document Base Issue Fee Transmittal Fee (Check) Sequence List y Pages 37 - 49 Other: Lisk (3.5")
,	